



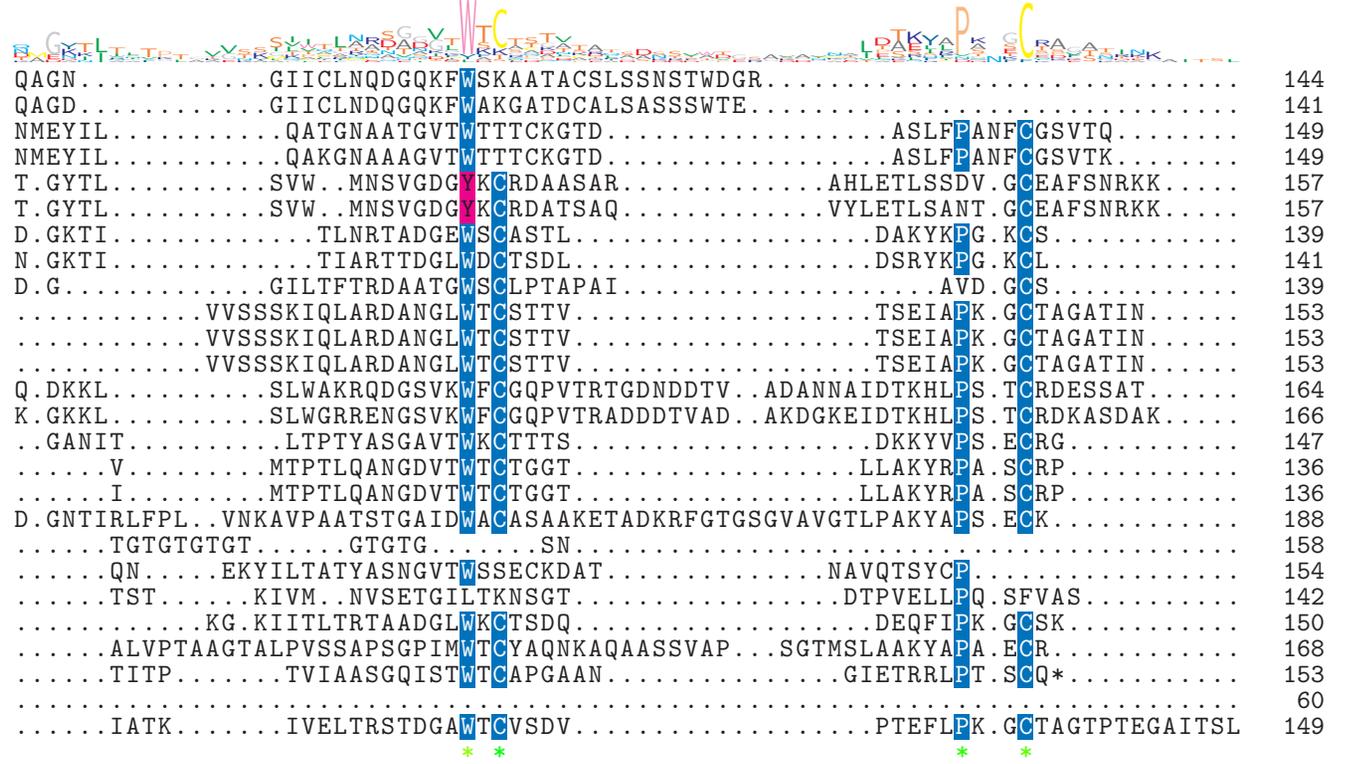
logo

NTDB id 1007 ACIAD RS15000 WP 004923844.1  
 NTDB id 1062 ABD1 RS15720 WP 000788345.1  
 NTDB id 1365 NTHI RS01955 WP 011271973.1  
 NTDB id 1354 HI 0299 AAC21963.1  
 NTDB id 1088 NMV RS07470 WP 173277181.1  
 NTDB id 1140 NGFG RS02440 WP 025455870.1  
 NTDB id 1197 PSJM300 03940 AFN76866.1  
 NTDB id 1204 PSJM300 03935 AFN76865.1  
 NTDB id 1292 VP RS12235 WP 005479693.1  
 NTDB id 1184 GTF74 RS02335 WP 000649326.1  
 NTDB id 1167 A1552VC RS11065 WP 000649326.1  
 NTDB id 1160 ABDM36 RS02330 WP 000649326.1  
 NTDB id 1109 OK783 RS10670 WP 157147416.1  
 NTDB id 1119 NGFG RS11465 WP 017147169.1  
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 NTDB id 1274 LPP RS09530 WP 011214168.1  
 NTDB id 1258 GCO85 RS09745 WP 014844212.1  
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 NTDB id 1191 AAC28468.1 484..945( )  
 NTDB id 994318 AAG092 RS07470 WP 110680823.1  
 NTDB id 1038 HON27 RS01510 WP 000993725.1  
 consensus

L...A..GLGNAASY.....P..VTCFAFYTLN.....LAVDSDNQGYVI..TATPISS.....TM 109  
 I...Q..SIYGSNVS.....P..LQCKALYTLA.....FTTL.NDSTWVL..TATPIAN.....TS 107  
 .....GCKNGIAAD.IITAKGYVK..SVTT...SNGAI..TV..KG....DGTLA 109  
 .....GCKNGIAAD.IKTAKGYVA..SVIT...QSCGI..TV..KG....NGTLA 109  
 ....SKLERF.....VSCYK...MN.PKIAEKYNV..SVHFVNKEKPR...YSL...VGVPKTG 112  
 ....SKLEIF.....VSCYK...MN.PKIAKKYSV..SVRFVDAEKPR...YRL...VGVNAG 112  
 T.....DECYGITDS.T....SY.C..DVDLDTA..ADCHI..ECTAKG...GNAGKF 108  
 S.....LPCFIGIGAS.T....NY.C..TVTLIAT.ATCSI..TCTTQN...GMPDRF 110  
 A.....QLGVDVAANDLGA....IDSALAG...GSPTI..TFTFDADS..S....I 109  
 GTAAG.....FTRLGTVEDMGDCIKIVIAP.....TASGA..LGCTI..KYTFDAG..... 114  
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 GTAAG.....FTRLGTVEDMGDCIKIVIAP.....TASGA..LGCTI..KYTFDAG..... 114  
 .....SAGVASA.STIKGKYVQKVEVA....KCVV..TAQMAST...GVNKEI 107  
 .....SAGVASPPTDIKGYVKEVEVK....NCVV..TATMLSS...GVNNEI 108  
 TPSTA.....GSSCVGVQE..ISASNATTNVATATCGAS.SACQI..IVTMDTTK..AK.... 113  
 ...QAA.....TCYV.SPAATPNV.....ASIAIG...ANCVI..TITYTAA..AGGGTI.. 104  
 ...QAA.....TCYV.SPAATPNV.....QSIAIG...ANCVI..TITYTAA..AGGGTI.. 104  
 ..MTAAAKAFNKTA.....AGGCAGGAAAAAGTQHASKYVK..SVKVTEA.SPWDI..TVAISATEANGIPTGL 127  
 CDSTANLGT.NAVATPGAITAAGAYSLDGTGSKFAVTA.TSVNKTFCFDGAKMGE..GTGATGACTFSTS..TGTGTG. 142  
 CHQTA.....N.....GIPAA.FTLNNLTVT...PAAGA..ASCAT..SITVNAA..NDKGPIK 119  
 ATA.....VTAA.DKVSGKYGD.AEIGGTA..PNCTI..TYTFKSS..GVSNKL.. 107  
 TGTEDATK..KEVP.....LCV..AADA.NKLGTIALK...PDPAD..GTADI..TLTFTMG..GAGPKN. 117  
 ....Q.....SDLS.....VCSVFTPT.KNVANLT..IAGTGTV...PCQI..TVTYTTA..AGGGT.L 113  
 ....A.....AALV.....ACNVIFDSA.NGLDGKYFAPGGVTVTP..DTCAI..NIAFDAG..ANAGKTM 117  
 ....K.....LS.....DVGFTAA.TSSVCATYSIDAFTETD..GACKI..TCTLKGK.....PK 105  
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 consensus



⊠ non conserved  
 ⊠ similar  
 ⊠ ≥ 50% conserved